In the Claims:

1. A method of DNA sequencing comprising the steps of:

(a) providing a template system comprising at least one nucleic acid molecule of unknown sequence hybridized to a primer oligonucleotide in the presence of a DNA polymerase with reduced exonuclease activity;

(b) contacting the template system with a single type of deoxyribonucleotide under conditions which allow extension of the primer by incorporation of at least one deoxyribonucleotide to the 3' end of the primer to form an extended primer;

(c) detecting whether extension of the primer has occurred;

(d) detecting the number of deoxyribonucleotides incorporated into the primer;

(e) removing unincorporated deoxyribonucleotide; and

(f) repeating steps (a) through (e) to determine the nucleotide sequence of the nucleic acid molecule.

2. The method of Claim 1 wherein the at least one deoxyribonucleotide includes a chemiluminescent moiety comprising detecting whether extension of the primer has occurred by detecting a chemiluminescent signal emitted by the chemiluminescent moiety, and further comprising removing the chemiluminescent moiety from the template system.

3. The method of Claim 1 wherein the at least one deoxyribonucleotide includes a fluorescent moiety comprising detecting whether extension of the primer has occurred by

detecting a fluorescent signal emitted by the fluorescent moiety, and further comprising removing the fluorescent moiety from the template system.

4. The method of Claim 1 wherein the at least one deoxyribonucleotide includes a fluorescent moiety comprising detecting whether extension of the primer has occurred by detecting a fluorescent signal emitted by the fluorescent moiety, and further comprising destroying the fluorescent signal without removal of the fluorescent moiety.

5. The method of claim 4 wherein the fluorescent moiety is destroyed by reaction with compounds capable of extracting an electron from the excited state of the fluorescent moiety.

6. The method of claim 5 wherein the compound is a diphenyliodonium salt.

7. The method of Claim 1 comprising detecting whether extension of the primer has occurred by detecting a change in the concentration of unincorporated deoxyribonucleotide.

8. The method of Claim 1, wherein incorporation of the at least one deoxyribonucleotide generates heat, comprising detecting whether extension of the primer has occurred by detecting the heat generated by said incorporation.

9. The method of Claim 8 wherein a thermopile is used to detect the generated heat.

10. The method of Claim 8 wherein a thermistor is used to detect the generated heat.

11. The method of Claim 1 wherein the template system further includes a buffer wherein incorporation of the at least one deoxyribonucleotide generates heat which is absorbed by said buffer and further comprising measuring the refractive index of the buffer.

12. The method of Claim 1 comprising detecting whether extension of the primer has occurred by detecting the concentration of pyrophosphate released by addition of a deoxyribonucleotide to the 3' end of the primer.

13. The method of Claim 12 wherein the concentration of pyrophosphate is detected by hydrolyzing the pyrophosphate and measuring heat generated by hydrolysis of the pyrophosphate.

14. The method of Claim 1 wherein the DNA polymerase is a T4 DNA polymerase with a substitution of amino acid residue Asp112 by Ala and Glu114 by Ala.

15. The method of Claim 11 wherein the DNA polymerase further comprises a T4 DNA polymerase with a substitution of amino acid residue Ile417 by Val.

16. A method of DNA sequencing comprising the steps of:

(a) providing a template system comprising at least one nucleic acid molecule of unknown sequence hybridized to a primer oligonucleotide in the presence of a exonuclease deficient DNA polymerase;

(b) contacting the template system with a single type of deoxyribonucleotide under conditions which allow extension of the primer

by incorporation of at least one deoxyribonucleotide to the 3' end of the primer to form an extended primer;

(c) detecting whether extension of the primer has occurred thereby identifying the deoxyribonucleotide added to the 3' end of the primer;

(d) detecting the number of deoxyribonucleotides incorporated into the primer;

(e) removing unincorporated deoxyribonucleotide;

(f) contacting the template system with a mixture including an exonuclease proficient DNA polymerase, an exonuclease deficient DNA polymerase and the identified deoxyribonucleotide of step (b);

(g) removing the mixture of step (f); and

(h) repeating steps (a) through (g) to determine the nucleotide sequence of the nucleic acid molecule.

17. The method of Claim 16 wherein the at least one deoxyribonucleotide includes a flourescent moiety comprising detecting whether extension of the primer has occurred by detecting a fluorescent signal emitted by the fluorescent moiety.

18. The method of Claim 16 wherein the at least one deoxyribonucleotide includes a fluorescent moiety comprising detecting whether extension of the primer has

occurred by detecting a fluorescent signal emitted by the fluorescent moiety, and further comprising destroying the fluorescent signal without removal of the fluorescent moiety.

19. The method of claim 18 wherein the fluorescent moiety is destroyed by reaction with compounds capable of extracting an electron from the excited state of the fluorescent moiety.

20. The method of claim 19 wherein the compound is a diphenyliodonium salt.

21. The method of Claim 16 wherein the at least one deoxyrilonucleotide includes a chemiluminescent moiety comprising detecting whether extension of the primer has occurred by detecting chemiluminescent signal emitted by the chemiluminescent moiety.

22. The method of Claim 16 comprising detecting whether extension of the primer has occurred by detecting a change in the concentration of unincorporated deoxyribonucleotide.

23. The method of Claim 16 wherein incorporation of the at least one deoxyribonucleotide generates heat comprising detecting whether extension of the primer has occurred by detecting heat generated by said incorporation.

24. The method of Claim 23 wherein a thermopile is used to detect the generated heat.

25. The method of Claim 23 wherein a thermistor is used to detect the generated heat.

26. The method of claim 16 wherein the template system further includes a buffer wherein incorporation of the at least one deoxyribonucleotide generates heat which is absorbed by said buffer and further comprising measuring the refractive index of the buffer.

27. The method of Claim 16 comprising detecting whether extension of the primer has occurred by detecting the concentration of pyrophosphate released by incorporation of a deoxyribonucleotide to the 3' end of the primer.

28. The method of Claim 27 wherein the concentration of pyrophosphate is detected by hydrolyzing the pyrophosphate and measuring the heat generated by hydrolysis of the pyrophosphate.

29. The method of Claim 16 wherein the exonuclease deficient DNA polymerase is a T4 DNA polymerase with a substitution of amino acid residue Asp112 by Ala and Glu114 by Ala.

30. The method of Claim 26 wherein the exonuclease deficient DNA polymerase further comprises a T4 DNA polymerase with a substitution of amino acid residue Ile417 by Val.

31. A method for removal of contaminating nucleotides from a solution comprising contacting said solution with immobilized DNA complementary to each of the three possibly contaminating nucleotides in the presence of primers and polymerase for a time sufficient to incorporate any contaminating nucleotides into DNA.

32 A method for discriminating between the in-phase and out-of-phase sequencing signals comprising:

(i) detecting and measuring error signals thereby determining the size of the trailing strand population;

(ii) between the 3' terminus of the trailing strand primers and the 3' terminus of the leading strand primers;

(iii) simulating the occurrence of an extension failure at a point upstream from the 3' terminus of the leading strands thereby predicting at each extension step the exact point in the sequence previously traversed by the leading strands to which the 3' termini of the trailing strands have been extended

(iv) predicting for each dNTP introduced the signal to be expected from correct extension of the trailing strands; and

(v) subtracting the predicted signal from the measured signal to yield a signal due only to correct extension of the leading strand population.